



#3

SEQUENCE LISTING

<110> Pharmacia AB

<120> Protein Cluster II

<130> 00404

<140> US/10/029,359

<141> 2001-12-21

<160> 6

<170> PatentIn version 3.0

<210> 1

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<212> DNA

<213> human

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<221> CDS

<222> (21)..(497)

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<221> misc_feature

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Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser
1 5 10

53

aaa tcc tgg ctg aat ttt tta acc ttc ctc tat gga tcg gca ata ggg
Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly
15 20 25

101

ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt
Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly
30 35 40

149

gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca
Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser
45 50 55

197

gat gat aat gga cag aat cat cta gga gga caa atg aac ttc aat gca
Asp Asp Asn Gly Gln Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala
60 65 70 75

245

gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc
Asp Ser Ser Gln Arg Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu
80 85 90

293

tat nag caa gtt aaa att ctt tgc tgg gtt atg aca ggc tct caa aac
Tyr Xaa Gln Val Lys Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn
95 100 105

341

cta cag aaa aag gcc aaa cat gtc aaa gct aca tgg gcc cag cgt tgt
Leu Gln Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys
110 115 120

389

cta aaa gta ttt ttt atg agt tca gaa gaa aat aaa gac ttc cgt gct
Leu Lys Val Phe Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala

437

125

130

135

gtg gga ttg aaa acc aaa gca ggc aga gat gag cta tac tgg aaa aca
Val Gly Leu Lys Thr Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr
140 145 150 155

485

att aac ctt ttc agtatgtt
Ile Asn Leu Phe

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20 25 30

Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
35 40 45

Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
50 55 60

Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
65 70 75 80

Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu Tyr xaa Gln Val Lys
85 90 95

Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn Leu Gln Lys Lys Ala
100 105 110

Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Leu Lys Val Phe Phe
115 120 125

Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala Val Gly Leu Lys Thr
130 135 140

Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr Ile Asn Leu Phe
145 150 155

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Thr	Gly	Val	Thr	Asp	Lys	Leu	Tyr	Gln	Lys	Met	Lys	Ile	Leu	Cys	Trp	
5								10							15	
att	atg	aca	gga	cct	caa	aat	cta	gaa	aaa	aag	atc	aga	cgc	atc	aga	153
Ile	Met	Thr	Gly	Pro	Gln	Asn	Leu	Glu	Lys	Lys	Ile	Arg	Arg	Ile	Arg	
20								25							30	
gat	aca	tgg	gcc	cag	ggt	tgc	aat	aaa	gcg	ttg	ttt	atg	agc	tca	aaa	201
Asp	Thr	Trp	Ala	Gln	Gly	Cys	Asn	Lys	Ala	Leu	Phe	Met	Ser	Ser	Lys	
35								40							45	
gaa	aat	aaa	gac	ttc	tct	act	gtg	gga	tta	cac	acc	aaa	gaa	gac	aga	249
Glu	Asn	Lys	Asp	Phe	Ser	Thr	Val	Gly	Leu	His	Thr	Lys	Glu	Asp	Arg	
50								55							65	
aac	caa	ctg	tcc	tgg	aaa	ata	gtt	aaa	gct	ttt	cta	tat	gct	cat	gac	297
Asn	Gln	Leu	Ser	Trp	Lys	Ile	Val	Lys	Ala	Phe	Leu	Tyr	Ala	His	Asp	
70								75							80	
cat	tat	ctg	gaa	tac	atg	gat	tgg	ttc	atg	aaa	gca	gat	gat	gat	ata	345
His	Tyr	Leu	Glu	Tyr	Met	Asp	Trp	Phe	Met	Lys	Ala	Asp	Asp	Asp	Ile	
85								90							95	
tgt	ata	tat	atc	aca	ttg	gac	aac	ttg	aaa	tgg	ctt	ctc	aca	aac	tat	393
Cys	Ile	Tyr	Ile	Thr	Leu	Asp	Asn	Leu	Lys	Trp	Leu	Leu	Thr	Asn	Tyr	
100								105							110	
aac	cct	gat	gaa	tcc	act	tac	ttt	ggg	aaa	aga	ttt	aag	cac	tgc	aga	441
Asn	Pro	Asp	Glu	Ser	Thr	Tyr	Phe	Gly	Lys	Arg	Phe	Lys	His	Cys	Arg	
115								120							125	
aaa	cag	gac	tac	atg	act	gga	gga	gca	gga	tat	gta	ctg	agc	aaa	gaa	489
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Trp Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile
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Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser
35 40 45

Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp
50 55 60

Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His
65 70 75 80

Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp
85 90 95

Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn
100 105 110

Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
115 120 125

Arg Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys
130 135 140

Glu
145

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1 5 10 15

tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat 97
Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
20 25 30

cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta 145
Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
35 40 45

gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac 193
Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
50 55 60

aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg 241
Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65 70 75 80

gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att 289
Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
85 90 95

aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg	337
Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp	
100 105 110	
ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg	385
Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg	
115 120 125	
tgg ctt ctt tca aaa tac gac cct gaa gaa ccc att tac ttt ggg aga	433
Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg	
130 135 140	
aga ttt aag cct tat gta aag cag ggc tac atg agt gga gga gca gga	481
Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly	
145 150 155 160	
tat gta cta agc aaa gaa gcc ttg aaa aga ttt gtt gat gca ttt aaa	529
Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys	
165 170 175	
aca gac aag tgt aca cat agt tcc tcc att gaa gac tta gca ctg ggg	577
Thr Asp Lys Cys Thr His Ser Ser Ile Glu Asp Leu Ala Leu Gly	
180 185 190	
aga tgc atg gaa att atg aat gta gaa gca gga gat tcc aga gat acc	625
Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr	
195 200 205	
att gga aaa gaa act ttt cat ccc ttt gtg cca gaa cac cat tta att	673
Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile	
210 215 220	
aaa ggt tat cta cct aga acg ttt tgg tac tgg aat tac aac tat tat	721
Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr	
225 230 235 240	
cct cct gta gag ggt cct ggt tgc tgc tct gat ctt gca gtt tct ttt	769
Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe	
245 250 255	
cac tat gtt gat tct aca acc atg tat gag tta gaa tac ctc gtt tat	817
His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr	
260 265 270	
cat ctt cgt cca tat ggt tat tta tac aga tat caa cct acc tta cct	865
His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro	
275 280 285	
gaa cgt ata cta aag gaa att agt caa gca aac aaa aat gaa gat aca	913
Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr	
290 295 300	
aaa gtg aag tta gga aat cct tgaaagaaaa tcatgaatga acaaaggtaa	964
Lys Val Lys Leu Gly Asn Pro	
305 310	
tatgtcttagc actgcactga aaaaggactt ctgcatttct gacatagaac actggaatcc	1024
cagtgaggaa ttcttaagtga acattcctta tagaaacctt tcacatgaat gactataaac	1084
tgaagcttta aatgagctgt gaagtgtgtt aaaatgtgtt ttgatacagt aatataaaa	1144
tatgtctata tatatgagga acttgtgttt tttaaatggg ggccaggtag aggaactaga	1204

aaagagattt tggtgcctgt tttctgacca tctgtgtat tgtcactgag aaactaaaat 1264
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Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
35 40 45

Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
50 55 60

Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65 70 75 80

Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
85 90 95

Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
100 105 110

Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
115 120 125

Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
130 135 140

Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
145 150 155 160

Tyr Val Leu S S Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
170 175

Thr Asp S S Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
180 185 190

Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
195 200 205

Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
210 215 220

Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
225 230 235 240

Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
245 250 255

His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
260 265 270

His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
275 280 285

Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
290 295 300

Lys Val Lys Leu Gly Asn Pro
305 310